

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/537,507
Source: PCP
Date Processed by STIC: 3/9/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/537,507</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleics J Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/537,507

DATE: 03/09/2006

TIME: 12:36:38

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\03092006\J537507.raw

3 <110> APPLICANT: Aarhus Universitet
 5 <120> TITLE OF INVENTION: Method for determining predisposition to
 manifestation of immune system
 6 related diseases

8 <130> FILE REFERENCE: P 706 DK 02
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/537,507
 C--> 10 <141> CURRENT FILING DATE: 2005-06-03

10 <160> NUMBER OF SEQ ID NOS: 8
 12 <170> SOFTWARE: PatentIn version 3.1
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 671
 16 <212> TYPE: PRT

17 <213> ORGANISM: Homo sapiens; mature MASP-2
 19 <400> SEQUENCE: 1

21 Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala
 22 1 5 10 15

25 Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
 26 20 25 30

29 Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
 30 35 40 45

33 Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
 34 50 55 60

37 Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
 38 65 70 75 80

41 Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
 42 85 90 95

45 Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
 46 100 105 110

49 Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
 50 115 120 125

53 Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
 54 130 135 140

57 Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
 58 145 150 155 160

61 Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln
 62 165 170 175

65 Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
 66 180 185 190

69 Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
 70 195 200 205

73 Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
 74 210 215 220

77 Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
 78 225 230 235 240

see item 2 on
1 Error Summary
sheet
Does Not Comply
Corrected Diskette Needed

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Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\03092006\J537507.raw

81 Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
82 245 250 255
85 Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
86 260 265 270
89 Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
90 275 280 285
93 Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
94 290 295 300
97 Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
98 305 310 315 320
101 Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
102 325 330 335
105 Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
106 340 345 350
109 Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
110 355 360 365
113 Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
114 370 375 380
117 Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
118 385 390 395 400
121 Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
122 405 410 415
125 Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
126 420 425 430
129 Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
130 435 440 445
133 Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
134 450 455 460
137 Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
138 465 470 475 480
141 Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
142 485 490 495
145 Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala
146 500 505 510
149 Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
150 515 520 525
153 Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
154 530 535 540
157 Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
158 545 550 555 560
161 Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
162 565 570 575
165 Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr
166 580 585 590
169 Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
170 595 600 605
173 Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
174 610 615 620
177 Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp

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Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\03092006\J537507.raw

178	625	630	635	640
181	Gly Ser Met Asn Cys	Gly Glu Ala Gly Gln	Tyr Gly Val Tyr Thr	Lys
182		645	650	655
185	Val Ile Asn Tyr Ile Pro Trp	Ile Glu Asn Ile Ile Ser Asp	Phe	
186		660	665	670
189	<210> SEQ ID NO: 2			
190	<211> LENGTH: 170			
191	<212> TYPE: PRT			
192	<213> ORGANISM: mature MAp-19 (human)			
194	<400> SEQUENCE: 2			
196	Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg	Leu Ala		
197	1	5	10	15
200	Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln	Glu Arg Arg Trp		
201	20	25	30	
204	Thr Leu Thr Ala Pro Pro Gly Tyr Arg	Leu Arg Leu Tyr Phe Thr His		
205	35	40	45	
208	Phe Asp Leu Glu Leu Ser His	Leu Cys Glu Tyr Asp Phe Val Lys	Leu	
209	50	55	60	
212	Ser Ser Gly Ala Lys Val	Leu Ala Thr Leu Cys Gly Gln	Glu Ser Thr	
213	65	70	75	80
216	Asp Thr Glu Arg Ala Pro Gly Lys Asp	Thr Phe Tyr Ser Leu Gly Ser		
217	85	90	95	
220	Ser Leu Asp Ile Thr Phe Arg Ser Asp	Tyr Ser Asn Glu Lys Pro Phe		
221	100	105	110	
224	Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp	Glu Cys Gln		
225	115	120	125	
228	Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His	Cys His Asn His		
229	130	135	140	
232	Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly	Tyr Val Leu His Arg		
233	145	150	155	160
236	Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu			
237	165	170		
240	<210> SEQ ID NO: 3			
241	<211> LENGTH: 2061			
242	<212> TYPE: DNA			
243	<213> ORGANISM: <i>cdNA MASP-2</i>			
245	<400> SEQUENCE: 3			
246	atgaggctgc tgaccctcct	gggccttctg tggggctcgg	tggccacccc	cttggggcccg
248	aagtggcctg aaccctgtgtt	cgggcgcctg	gcatcccccg	gttccagg ggagtatgcc
250	aatgaccagg	agcggcgctg	gaccctgact	gcaccccccgt
252	tccacccact	tgcaccttgg	ctctccac	ctctgcgagt
254	tcgggggcca	aggtgctggc	cacgctgtgc	ggcaggaga
256	cctggcaagg	acactttcta	ctcgctggc	gcacagacac
258	tactccaacg	agaagccgtt	cacggggttc	ggagccttct
260	gagtgccagg	tggcccccggg	agaggcgccc	acctgcgacc
262	ggcggtttct	actgctcctg	ccgcgcaggg	accactgcca
264	tccggccctgt	gctccggcca	ggtttcacc	cagaggctctg
266	tacccacggc	cgtatcccaa	actctccagt	ggagagctcag
268	ttcagtgtca	ttctggactt	tgtggagtcc	gcatcagccgt
			ggacacacccc	tgaaaccctg
				720

*invalid <213> response. See item 10
on Error Summary
sheet.*

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Input Set : A:\PTO.KD.txt
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270	tgtccctacg	actttctcaa	gattcaaaca	gacagagaag	aacatggccc	attctgtggg	780
272	aagacattgc	cccacaggat	tgaaacaaaa	agcaacacgg	tgaccatcac	ctttgtcaca	840
274	gatgaatcag	gagaccacac	aggcttggaa	atccactaca	cgagcacagc	gcagcctgc	900
276	ccttatccga	tggcgccacc	taatggccac	gtttcacctg	tgcaagccaa	atacatcctg	960
278	aaagacagct	tctccatctt	ttgcgagact	ggctatgagc	ttctgcaagg	tcacttgccc	1020
280	ctgaaaatcct	ttactgcagt	ttgtcagaaa	gatggatctt	gggaccggcc	aatgcccgcg	1080
282	tgcagcattg	ttgactgtgg	ccctcctgat	gatctaccca	gtggccgagt	ggagtagatc	1140
284	acaggtcctg	gagtgaccac	ctacaaagct	gtgattcagt	acagctgtga	agagaccttc	1200
286	tacacaatga	aagtgaatga	tggtaaatat	gtgtgtgagg	ctgatggatt	ctggacgagc	1260
288	tccaaaggag	aaaaatcact	cccagtcgt	gagcctgttt	gtggactatc	agcccgacaca	1320
290	acaggagggc	gtatatatgg	aggcggaaaag	gcaaaacctg	gtgattttcc	ttggcaagtc	1380
292	ctgatattag	gtggaaccac	agcagcaggt	gcactttat	atgacaactg	ggtcctaaca	1440
294	gctgctcatg	ccgtctatga	gcaaaaacat	gatgcacatccg	ccctggacat	tcgaatgggc	1500
296	accctgaaaa	gactatcacc	tcattataca	caagcctggt	ctgaagctgt	ttttatacat	1560
298	gaaggttata	ctcatgatgc	tggctttgac	aatgacatag	cactgattaa	attgaataac	1620
300	aaagttgtaa	tcaatagcaa	catcagcct	atttgcgtgc	caagaaaaga	agctgaatcc	1680
302	tttatgagga	cagatgacat	tggactgca	tctggatggg	gattaaccca	aaggggttt	1740
304	cttgctagaa	atctaattgt	tgtcgacata	ccgatttttg	accatcaaaa	atgtactgct	1800
306	gcatatgaaa	agccacccta	tccaagggg	agtgtactg	ctaacatgct	tttgctggc	1860
308	ttagaaagt	ggggcaagga	cagctgcaga	ggtgacagcg	gaggggca	ggtgtttcta	1920
310	gatagtgaaa	cagagaggt	gtttgtggg	ggaatagtgt	cctggggttc	catgaattgt	1980
312	ggggaaagcag	gtcagttatgg	agtctacaca	aaagtttata	actatattcc	ctggatcgag	2040
314	aacataatta	gtgattttta	a				2061
317	<210>	SEQ ID NO:	4				
318	<211>	LENGTH:	558				
319	<212>	TYPE:	DNA				
320	<213>	ORGANISM:	CDNA MAp-19	same env			
322	<400>	SEQUENCE:	4				
323	atgaggctgc	tgaccctcct	gggccttctg	tgtggctcg	tggccacccc	cttggggccc	60
325	aagtggctg	aacctgtgtt	cgggcgcctg	gcatcccccg	gtttccagg	ggagtagatgcc	120
327	aatgaccagg	agcggcgctg	gaccctgact	gcacccccc	gctaccgcct	gcgcctctac	180
329	ttcacccact	tcgaccttgg	gctctccac	ctctgcgagt	acgacttcgt	caagctgagc	240
331	tcgggggcca	aggtgcttgc	cacgctgtgc	gggcaggaga	gcacagacac	ggagcgggccc	300
333	cctggcaagg	acactttcta	ctcgctggc	tccagcctgg	acattacctt	ccgctccgac	360
335	tactccaacg	agaagccgtt	cacggggttc	gaggccttct	atgcagccga	ggacattgac	420
337	gagtgccagg	tggccccgg	agagggcccc	acctgcgacc	accactgcca	caaccacctg	480
339	ggcggtttct	actgctctg	ccgcgcaggg	tacgtctgc	acctaatacaa	gcgcacactgc	540
341	tcagagcaga	gcctctag					558
344	<210>	SEQ ID NO:	5				
345	<211>	LENGTH:	21				
346	<212>	TYPE:	DNA				
347	<213>	ORGANISM:	upper PCR primer				
349	<400>	SEQUENCE:	5				
350	gcgagttacga	tttcgtcaag	g				21
353	<210>	SEQ ID NO:	6				
354	<211>	LENGTH:	21				
355	<212>	TYPE:	DNA				
356	<213>	ORGANISM:	lower PCR primer				
358	<400>	SEQUENCE:	6				

RAW SEQUENCE LISTING
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Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\03092006\J537507.raw

359 ctcggctgca tagaaggcct c	21
362 <210> SEQ ID NO: 7	
363 <211> LENGTH: 21	
364 <212> TYPE: DNA	
365 <213> ORGANISM: <i>Upper PCR primer</i>	
367 <400> SEQUENCE: 7	
368 ccagaccttt ggaaagttag c	21
371 <210> SEQ ID NO: 8	
372 <211> LENGTH: 21	
373 <212> TYPE: DNA	
374 <213> ORGANISM: <i>Lower PCR primer</i>	
376 <400> SEQUENCE: 8	
377 ggctcaagtt ccaagtattg c	21

VERIFICATION SUMMARY DATE: 03/09/2006
PATENT APPLICATION: US/10/537,507 TIME: 12:36:39

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\03092006\J537507.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date